

DNA REPORT WRITING-SEXUAL ASSAULT SCENARIOS

A. SCOPE

The laboratory report must communicate both the analytical results and the conclusions of the examiner, conveying the essence of the expert testimony in court. The notes and other documentation must support the conclusions of the examiner. Decisions may be made by police officers, attorneys and the courts based on the report alone without examiner clarification, so the report should be able to stand alone. The report must contain the information required in the Laboratory Quality Assurance Manual and the FBI DNA Quality Assurance Audit Document.

Typical casework reporting should follow the recommended reporting statements, as appropriate. It is recognized that not every situation can be represented by these statements and that it may be necessary to modify the statements to accurately reflect the results.

B. REPORTING STATEMENTS

B.1 REPORTING SEXUAL ASSAULT SCENARIOS

NOTE: Any statistics reported using the following statements should have four significant figures.

B.1.1 Scenario Example: A differential extraction was performed and there is carryover of the known female DNA into the sperm fraction. The female contribution can be subtracted from the sperm fraction. Results may be reported as:

Reporting Statement: Comparison of DNA profiles showed the DNA profile obtained from the **NAME** reference sample to be the same as the (male) DNA profile obtained from the sperm fraction from the vaginal swab. The estimated frequency of this matching DNA profile is approximately 1 in **MOST COMMON STATISTIC (7.356 quintillion (7.356 x 10¹⁸))** individuals. Based upon these results, it is reasonable to conclude that **NAME** is the source of this DNA profile. **NAME** is excluded as the source of the DNA profile obtained from **EVIDENCE**.

B.1.2 Scenario Example: No differential extraction was performed and the sample is a skin swab such as a neck or breast swab or a differential extraction was performed and this is an epithelial fraction such as that from a penile swab. Statistics are greater than 1 in 8 trillion in all three populations.

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Reporting Statement: Comparison of DNA profiles showed the DNA profile obtained from the **NAME** reference sample to be the same as the DNA profile foreign to **NAME** from the **EVIDENCE**. The estimated frequency of this matching DNA profile is approximately 1 in **MOST COMMON STATISTIC** (7.356 quintillion (7.356×10^{18})) individuals. Based upon these results, it is reasonable to conclude that **NAME** is the source of this DNA profile. **NAME** is excluded as the source of the DNA profile obtained from **EVIDENCE**.

B.1.3 Scenario Example: No differential extraction was performed and the sample is a skin swab such as a neck or breast swab or a differential extraction was performed and this is an epithelial fraction such as that from a penile swab. Statistics are less than 1 in 8 trillion in all three populations.

Reporting Statement: Comparison of DNA profiles showed the DNA profile obtained from the **NAME** reference sample to be the same as the DNA profile foreign to **NAME** from the **EVIDENCE**. The estimated frequency of this matching DNA profile is approximately 1 in **MOST COMMON STATISTIC** (7.356 billion (7.356×10^9)) individuals. Based upon these results, **NAME** cannot be excluded as the source of this DNA profile. **NAME** is excluded as the source of the DNA profile obtained from **EVIDENCE**.

B.1.4 Scenario Example: A differential extraction was performed on **EVIDENCE STAIN**. A single source DNA profile is obtained in the sperm fraction. A three person mixed DNA profile is obtained in the epithelial fraction. The single source profile obtained in the sperm fraction (Profile X) accounts for a significant portion of the dominant alleles in the mixed DNA profile in the epithelial fraction. This profile can be subtracted from the mixed DNA profile leaving a single source dominant DNA profile and a minor DNA profile. Profile X does not have to be accounted for as being in the epithelial fraction in the report but it must be indicated as such in the table. The following language can then be used when source statistics are obtained for the dominant DNA profile and a low level minor:

Reporting Statement: Comparison of DNA profiles showed the DNA profile from the **NAME** reference sample to be the same as the DNA profile from the sperm fraction from the **EVIDENCE STAIN**. The estimated frequency of this matching DNA profile is approximately 1 in **MOST COMMON STATISTIC (7.356 quintillion (7.356×10^{18}))** individuals. Based upon these results, it is reasonable to conclude that **NAME** is the source of this DNA profile. **NAME** is excluded as the source of the DNA profile obtained from **EVIDENCE**.

The results from the epithelial fraction from the **EVIDENCE** indicate at least two sources of DNA. Comparison of DNA profiles showed the DNA profile from the

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NAME reference sample to be the same as the dominant DNA profile from the epithelial fraction from the **EVIDENCE**. The estimated frequency of this matching DNA profile is approximately 1 in **MOST COMMON STATISTIC (7.356 quintillion (7.356 x 10¹⁸))** individuals. Based upon these results, it is reasonable to conclude that **NAME** is the source of this dominant DNA profile. **NAME** is excluded as the source of the dominant DNA profile obtained from **EVIDENCE**. Due to a low level of DNA, no conclusions are being offered for the **minor DNA profile / minor DNA results**.

B.1.5 Scenario Example: A differential extraction was performed due to case information. No spermatozoa were identified during Primary Examination, which could be due to the small sampling size or due to the lack of spermatozoa. A male profile was obtained in both the sperm and epithelial fraction (differing stats). Both fractions need to be reported for whatever reason.

Reporting Statement: *This statement can be added to the end of the report.*
A “sperm fraction” denotes one of two fractions obtained during the DNA analysis process used to obtain DNA from spermatozoa; this process is utilized if spermatozoa are suspected of being present in a sample. This terminology does not imply the presence or absence of spermatozoa in this case.

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